

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 23, 2003, 11:53:01 ; Search time 354 Seconds
(without alignments)

2437.305 Million cell updates/sec

Title: US-10-045-594D-2

Perfect score: 1395

Sequence: 1 MLSHNTWQKQKQKQATLKM.....PIVITTEPDDTTPESDL 264

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1455
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=2000000000 -USER=US10045594 -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0
-ICPU=6 -ICPU3=3 -NO MAP -LARGESQUEW -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgm2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgm2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgm2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgm2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgm2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgm2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgm2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgm2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgm2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 16: /cgm2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 17: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1395	100.0	1119	13	US-10-098-841-286 Sequence 286, App

2	527	37.8	434	11	US-09-918-995-3415	Sequence 3415, Ap
3	509	36.5	1295	10	US-09-983-965-258	Sequence 258, App
4	371.5	26.6	1295	14	US-10-037-270-917	Sequence 917, App
5	159	11.4	814	12	US-10-257-826A-277	Sequence 277, App
6	101	7.2	60	12	US-09-908-975-23712	Sequence 23712, A
7	100	7.2	5519	9	US-09-764-869-1329	Sequence 1319, Ap
8	100	7.2	5519	9	US-09-764-869-2240	Sequence 2240, Ap
9	100	7.2	5519	14	US-10-091-504-1319	Sequence 1319, Ap
10	100	7.2	5519	14	US-10-091-504-2240	Sequence 2240, Ap
11	99.5	7.1	9025608	14	US-10-156-761-1	Sequence 1, App-1
12	98	7.0	828	12	US-10-360-828-62	Sequence 62, App-1
13	97	7.0	2287	9	US-09-287-849-1	Sequence 1, App-1
14	97	7.0	2287	12	US-10-359-460-1	Sequence 1, App-1
15	97	7.0	2287	12	US-10-098-732A-15	Sequence 15, App-1
16	96.5	6.9	5360	12	US-10-304-708-65	Sequence 65, App-1
17	96.5	6.9	5360	12	US-10-311-455-1909	Sequence 1909, Ap
18	96	6.9	1797	9	US-09-287-849-25	Sequence 25, App-1
19	96	6.9	1797	12	US-10-359-460-25	Sequence 25, App-1
20	96	6.9	1797	12	US-10-098-732A-19	Sequence 19, App-1
21	96	6.9	1801	9	US-09-287-849-21	Sequence 21, App-1
22	96	6.9	1801	12	US-10-359-460-21	Sequence 21, App-1
23	96	6.9	2190	12	US-10-098-732A-17	Sequence 17, App-1
24	96	6.9	2808	12	US-10-098-732A-64	Sequence 64, App-1
25	96	6.9	3058	12	US-10-084-843-106	Sequence 106, App
26	96	6.9	3058	12	US-10-193-002-101	Sequence 101, App
27	96	6.9	3058	12	US-10-098-732A-13	Sequence 13, App-1
28	96	6.9	3324	10	US-09-954-456-1171	Sequence 1171, Ap
29	96	6.9	53500	12	US-09-953-348-76	Sequence 76, App-1
30	96	6.9	53500	14	US-10-267-255-76	Sequence 76, App-1
31	96	6.9	75216	15	US-10-080-170-646	Sequence 646, App-1
32	95.5	6.8	2148	12	US-10-171-404A-43	Sequence 43, App-1
33	95	6.8	6135	12	US-10-311-455-1545	Sequence 1545, Ap
34	95	6.8	14353	12	US-10-311-455-2407	Sequence 2407, Ap
35	94.5	6.8	2244	10	US-09-938-842A-2448	Sequence 2448, Ap
36	94	6.7	6077	12	US-10-311-455-1219	Sequence 1219, Ap
37	94	6.7	9025608	14	US-10-156-761-1	Sequence 1, App-1
38	93.5	6.7	2518	10	US-09-771-161A-53	Sequence 53, App-1
39	93.5	6.7	2988	12	US-10-354-358-73	Sequence 73, App-1
40	93.5	6.7	2988	14	US-10-171-581-366	Sequence 366, App
41	93.5	6.7	5898	12	US-10-311-455-1913	Sequence 1913, Ap
42	93.5	6.7	5898	14	US-10-240-453-203	Sequence 203, App
43	93.5	6.7	5898	14	US-10-239-676-179	Sequence 179, App
44	93	6.7	3356	12	US-09-814-353-19824	Sequence 19824, A
45	93	6.7	8588	10	US-09-816-669A-13	Sequence 13, App-1

ALIGNMENTS

RESULT 1

US-10-098-841-286 Application US/10098841
Sequence 286, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wehman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Qian, Xiaohong B.
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
CURRENT APPLICATION NUMBER: US/10/098,841

```

CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,942 not pub
PRIOR FILING DATE: 2000-06-20 not pub
PRIOR APPLICATION NUMBER: 09/582,317 not pub
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725 not pub
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ IDS NOS: 331

```

```

; SOFTWARE: pf_FFL_genes version 1.0
; SEQ ID NO: 286
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(922)
US-10-098-841-286

Alignment Scores:
Pred. No.: 5,39e-155
Score: 1395.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13

Length: 1119
Matches: 264
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-045-594D-2 (1-264) x US-10-098-841-286 (1-1119)

```

Db	788	TCTTTGTC	CAATCC	CTTCT	TGGCAG	CGGTCT	TTAAT	AGGACT	CTCTA	AGGATG	CGATA	847
Qy	241	SerGlu	AsnIle	ProIle	ValIle	ThrGlu	ProThr	AspAsp	ThrThr	ValPro	Glu	260
Db	848	TCTGAGA	TATTC	TATAG	TGTAA	CAAC	CCGAC	CTAC	AGAT	TATCC	CTGTAC	CGAA
Qy	261	SerGlu	AspLeu	264								
Db	908	TCAGA	GACCTA	919								

```

RESULT 2
US-09-918-995-3415
; Sequence 3415, Application US/09918995
; Publication NO. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3415
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-3415

```

Alignment Scores:	
Fred. No.:	5.77e-53
Score:	527.00
Length:	434
Percent Similarity:	100.00%
Matches:	103
Best Local Similarity:	100.00%
Conservative:	0
Mismatches:	0
Query Match:	37.78%
Indels:	0
DB:	11
Gaps:	0

US-10-045-594D-2 (1-264) x US-09-918-995-3415 (1-434);

QY	1	MetLeuSerHisAsnThrMetMetLeuGlnArgLysGlnGlnAlaThrAlaIleMetLys	20
DB	124	ATGCTATCACATAATACTATCATCAAGCAGAGAAAACAGCAAGCAACAGCCATCATGAG	183
QY	21	GluValHisGlyAsnAspValAspGlyMetAspLeuGlyLysLysValSerIleProArg	40
DB	184	GAAGTCCATGGAAATGATTGATGGCATGGACCTGGGCAAAAAGGTCAGCATCCCCAGA	243
QY	41	AspIleMetLeuGluLeuSerHisLeuSerAsnArgGlyAlaArgLeuPheLysMet	60
DB	244	GACATCATGTTGGAGAAGAAATTATCCCATCTCAGTAACCGTGTCGCCAGGCTATTTAAGATG	303
QY	61	ArgGlnArgArgSerAspLysTyrThrPheGluAsnPheGlnTyrGlnSerArgAlaGln	80
DB	304	CGTCAAGAAGATCTGACAAATACACATTTGAAAATTTCCAGATATCAAATCTAGAGCACAA	363
QY	81	IleAsnHisSerIleAlaMetGluAsnGlyLysValAspGlySerAsnLeuGluGlyGly	100
DB	364	ATAAATACAGTATTGCTATGCAGAAATGGGAAAGTGGATGGAAGTAACTTGGAAAGTGGT	423
QY	101	SerGlnGln	103
DB	424	TCCAGCAA	432

RESULT 3
US-09-983-965-258
: Sequence 258, Application US/09983965
: Patent No. US20026137160A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Wengbing